

# SEQUENCE LISTING

<110> Wong, Justin  
Winter, Jill  
Lalehzadeh, Guita  
Warne, Robert

<120> Compositions and Methods of Therapy for  
Cancers Characterized by Expression of the Tumor-Associated  
Antigen MN/CA IX

<130> PP19155.002/035784/267827

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1  
<211> 1380  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(1380)

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cct gct cca ggc ctc act gtg caa ctg ctg ctg tca ctg ctg ctt ctg 96
Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu
20 25 30

atg cct gtc cat ccc cag agg ttg ccc cgg atg cag gag gat tcc ccc 144
Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
35 40 45

ttg gga gga ggc tct tct ggg gaa gat gac cca ctg ggc gag gag gat 192
Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
50 55 60

ctg ccc agt gaa gag gat tca ccc aga gag gag gat cca ccc gga gag 240
Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
65 70 75 80

gag gat cta cct gga gag gag gat cta cct gga gag gag gat cta cct 288
Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
85 90 95

gaa gtt aag cct aaa tca gaa gaa gag ggc tcc ctg aag tta gag gat 336
Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp
100 105 110

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cta cct act gtt gag gct cct gga gat cct caa gaa ccc cag aat aat	384
Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn	
115 120 125	
gcc cac agg gac aaa gaa ggg gat gac cag agt cat tgg cgc tat gga	432
Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly	
130 135 140	
ggc gac ccg ccc tgg ccc cgg gtg tcc cca gcc tgc gcg ggc cgc ttc	480
Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe	
145 150 155 160	
cag tcc ccg gtg gat atc cgc ccc cag ctc gcc gcc ttc tgc ccg gcc	528
Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala	
165 170 175	
ctg cgc ccc ctg gaa ctc ctg ggc ttc cag ctc ccg ccg ctc cca gaa	576
Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu	
180 185 190	
ctg cgc ctg cgc aac aat ggc cac agt gtg caa ctg acc ctg cct cct	624
Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro	
195 200 205	
ggg cta gag atg gct ctg ggt ccc ggg cgg gag tac cgg gct ctg cag	672
Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln	
210 215 220	
ctg cat ctg cac tgg ggg gct gca ggt cgt ccg ggc tcg gag cac act	720
Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr	
225 230 235 240	
gtg gaa ggc cac cgt ttc cct gcc gag atc cac gtg gtt cac ctc agc	768
Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser	
245 250 255	
acc gcc ttt gcc aga gtt gac gag gcc ttg ggg cgc ccg gga ggc ctg	816
Thr Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu	
260 265 270	
gcc gtg ttg gcc gcc ttt ctg gag gag ggc ccg gaa gaa aac agt gcc	864
Ala Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala	
275 280 285	
tat gag cag ttg ctg tct cgc ttg gaa gaa atc gct gag gaa ggc tca	912
Tyr Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser	
290 295 300	
gag act cag gtc cca gga ctg gac ata tct gca ctc ctg ccc tct gac	960
Glu Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp	
305 310 315 320	
ttc agc cgc tac ttc caa tat gag ggg tct ctg act aca ccg ccc tgt	1008
Phe Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys	
325 330 335	

gcc cag ggt gtc atc tgg act gtg ttt aac cag aca gtg atg ctg agt	1056
Ala Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser	
340 345 350	
gct aag cag ctc cac acc ctc tct gac acc ctg tgg gga cct ggt gac	1104
Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp	
355 360 365	
tct cgg cta cag ctg aac ttc cga gcg acg cag cct ttg aat ggg cga	1152
Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg	
370 375 380	
gtg att gag gcc tcc ttc cct gct gga gtg gac agc agt cct cgg gct	1200
Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala	
385 390 395 400	
gct gag cca gtc cag ctg aat tcc tgc ctg gct gct ggt gac atc cta	1248
Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu	
405 410 415	
gcc ctg gtt ttt ggc ctc ctt ttt gct gtc acc agc gtc gcg ttc ctt	1296
Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu	
420 425 430	
gtg cag atg aga agg cag cac aga agg gga acc aaa ggg ggt gtg agc	1344
Val Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser	
435 440 445	
tac cgc cca gca gag gta gcc gag act gga gcc tag	1380
Tyr Arg Pro Ala Glu Val Ala Glu Thr Gly Ala *	
450 455	

<210> 2  
 <211> 459  
 <212> PRT  
 <213> Homo sapiens

<400> 2

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Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Ser Leu Leu Leu	
20 25 30	
Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro	
35 40 45	
Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp	
50 55 60	
Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu	
65 70 75 80	
Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro	
85 90 95	
Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp	
100 105 110	
Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn	
115 120 125	
Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly	
130 135 140	

Gly	Asp	Pro	Pro	Trp	Pro	Arg	Val	Ser	Pro	Ala	Cys	Ala	Gly	Arg	Phe	145	150	155	160
Gln	Ser	Pro	Val	Asp	Ile	Arg	Pro	Gln	Leu	Ala	Ala	Phe	Cys	Pro	Ala	165	170	175	
Leu	Arg	Pro	Leu	Glu	Leu	Leu	Gly	Phe	Gln	Leu	Pro	Pro	Leu	Pro	Glu	180	185	190	
Leu	Arg	Leu	Arg	Asn	Asn	Gly	His	Ser	Val	Gln	Leu	Thr	Leu	Pro	Pro	195	200	205	
Gly	Leu	Glu	Met	Ala	Leu	Gly	Pro	Gly	Arg	Glu	Tyr	Arg	Ala	Leu	Gln	210	215	220	
Leu	His	Leu	His	Trp	Gly	Ala	Ala	Gly	Arg	Pro	Gly	Ser	Glu	His	Thr	225	230	235	240
Val	Glu	Gly	His	Arg	Phe	Pro	Ala	Glu	Ile	His	Val	Val	His	Leu	Ser	245	250	255	
Thr	Ala	Phe	Ala	Arg	Val	Asp	Glu	Ala	Leu	Gly	Arg	Pro	Gly	Gly	Leu	260	265	270	
Ala	Val	Leu	Ala	Ala	Phe	Leu	Glu	Glu	Gly	Pro	Glu	Glu	Asn	Ser	Ala	275	280	285	
Tyr	Glu	Gln	Leu	Leu	Ser	Arg	Leu	Glu	Glu	Ile	Ala	Glu	Glu	Gly	Ser	290	295	300	
Glu	Thr	Gln	Val	Pro	Gly	Leu	Asp	Ile	Ser	Ala	Leu	Leu	Pro	Ser	Asp	305	310	315	320
Phe	Ser	Arg	Tyr	Phe	Gln	Tyr	Glu	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	325	330	335	
Ala	Gln	Gly	Val	Ile	Trp	Thr	Val	Phe	Asn	Gln	Thr	Val	Met	Leu	Ser	340	345	350	
Ala	Lys	Gln	Leu	His	Thr	Leu	Ser	Asp	Thr	Leu	Trp	Gly	Pro	Gly	Asp	355	360	365	
Ser	Arg	Leu	Gln	Leu	Asn	Phe	Arg	Ala	Thr	Gln	Pro	Leu	Asn	Gly	Arg	370	375	380	
Val	Ile	Glu	Ala	Ser	Phe	Pro	Ala	Gly	Val	Asp	Ser	Ser	Pro	Arg	Ala	385	390	395	400
Ala	Glu	Pro	Val	Gln	Leu	Asn	Ser	Cys	Leu	Ala	Ala	Gly	Asp	Ile	Leu	405	410	415	
Ala	Leu	Val	Phe	Gly	Leu	Leu	Phe	Ala	Val	Thr	Ser	Val	Ala	Phe	Leu	420	425	430	
Val	Gln	Met	Arg	Arg	Gln	His	Arg	Arg	Gly	Thr	Lys	Gly	Gly	Val	Ser	435	440	445	
Tyr	Arg	Pro	Ala	Glu	Val	Ala	Glu	Thr	Gly	Ala						450	455		

<210> 3  
 <211> 540  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Coding sequence for human CA IX proteoglycan  
 domain construct

<221> CDS  
 <222> (1) ... (540)

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Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
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ctt gct cca ggc ctc act gtg caa ctg ctg ctg tca ctg ctg ctt ctg 96
Leu Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu
20 25 30

atg cct gtc cat ccc cag agg ttg ccc cgg atg cag gag gat tcc ccc 144
Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
35 40 45

ttg gga gga ggc tct tct ggg gaa gat gac cca ctg ggc gag gag gat 192
Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
50 55 60

ctg ccc agt gaa gag gat tca ccc aga gag gag gat cca ccc gga gag 240
Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
65 70 75 80

gag gat cta cct gga gag gag gat cta cct gga gag gag gat cta cct 288
Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
85 90 95

gaa gtt aag cct aaa tca gaa gaa gag ggc tcc ctg aag tta gag gat 336
Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp
100 105 110

cta cct act gtt gag gct cct gga gat cct caa gaa ccc cag aat aat 384
Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn
115 120 125

gcc cat agg agc tcg agc atc cta gcc ctg gtt ttt ggc ctc ctt ttt 432
Ala His Arg Ser Ser Ser Ile Leu Ala Leu Val Phe Gly Leu Leu Phe
130 135 140

gct gtc acc agc gtc gcg ttc ctt gtg cag atg aga agg cag cac aga 480
Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln His Arg
145 150 155 160

agg gga acc aaa ggg ggt gtg agc tac cgc cca gca gag gta gcc gag 528
Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val Ala Glu
165 170 175

act gga gcc tag 540
Thr Gly Ala *

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<210> 4
<211> 179
<212> PRT
<213> Artificial Sequence

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<220>

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<223> Polypeptide encoded by coding sequence for human  
CA IX proteoglycan domain construct

<400> 4

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Leu Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu
 20          25          30
Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
 35          40          45
Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
 50          55          60
Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
 65          70          75          80
Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
 85          90          95
Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp
100          105          110
Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn
115          120          125
Ala His Arg Ser Ser Ser Ile Leu Ala Leu Val Phe Gly Leu Leu Phe
130          135          140
Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln His Arg
145          150          155          160
Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val Ala Glu
165          170          175
Thr Gly Ala

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<210> 5

<211> 1089

<212> DNA

<213> Artificial Sequence

<220>

<223> Coding sequence for human CA IX carbonic anhydrase  
domain construct

<221> CDS

<222> (1)...(1089)

<400> 5

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Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
 1          5          10          15

cct gct cca ggc ctc act gtg caa ctg ctg ctg tca ctg ctg ctt ctg      96
Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu
 20          25          30

atg cct gtc cat ccc ggg gat gac cag agt cat tgg cgc tat gga ggc      144
Met Pro Val His Pro Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly
 35          40          45

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gac ccg ccc tgg ccc cgg gtg tcc cca gcc tgc gcg ggc cgc ttc cag	192
Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln	
50 55 60	
tcc ccg gtg gat atc cgc ccc cag ctc gcc gcc ttc tgc ccg gcc ctg	240
Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu	
65 70 75 80	
cgc ccc ctg gaa ctc ctg ggc ttc cag ctc ccg ccg ctc cca gaa ctg	288
Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu	
85 90 95	
cgc ctg cgc aac aat ggc cac agt gtg caa ctg acc ctg cct cct ggg	336
Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly	
100 105 110	
cta gag atg gct ctg ggt ccc ggg cgg gag tac cgg gct ctg cag ctg	384
Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu	
115 120 125	
cat ctg cac tgg ggg gct gca ggt cgt ccg ggc tcg gag cac act gtg	432
His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val	
130 135 140	
gaa ggc cac cgt ttc cct gcc gag atc cac gtg gtt cac ctc agc acc	480
Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr	
145 150 155 160	
gcc ttt gcc aga gtt gac gag gcc ttg ggg cgc ccg gga ggc ctg gcc	528
Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala	
165 170 175	
gtg ttg gcc gcc ttt ctg gag gag ggc ccg gaa gaa aac agt gcc tat	576
Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr	
180 185 190	
gag cag ttg ctg tct cgc ttg gaa gaa atc gct gag gaa ggc tca gag	624
Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu	
195 200 205	
act cag gtc cca gga ctg gac ata tct gca ctc ctg ccc tct gac ttc	672
Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe	
210 215 220	
agc cgc tac ttc caa tat gag ggg tct ctg act aca ccg ccc tgt gcc	720
Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala	
225 230 235 240	
cag ggt gtc atc tgg act gtg ttt aac cag aca gtg atg ctg agt gct	768
Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala	
245 250 255	
aag cag ctc cac acc ctc tct gac acc ctg tgg gga cct ggt gac tct	816
Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser	
260 265 270	

cgg cta cag ctg aac ttc cga gcg acg cag cct ttg aat ggg cga gtg	864
Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val	
275 280 285	
att gag gcc tcc ttc cct gct gga gtg gac agc agt cct cgg gct gct	912
Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala	
290 295 300	
gag cca gtc cag ctg aat tcc tgc ctg gct gct ggt gac atc cta gcc	960
Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala	
305 310 315 320	
ctg gtt ttt ggc ctc ctt ttt gct gtc acc agc gtc gcg ttc ctt gtg	1008
Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val	
325 330 335	
cag atg aga agg cag cac aga agg gga acc aaa ggg ggt gtg agc tac	1056
Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr	
340 345 350	
cgc cca gca gag gta gcc gag act gga gcc tag	1089
Arg Pro Ala Glu Val Ala Glu Thr Gly Ala *	
355 360	

<210> 6

<211> 362

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide encoded by coding sequence for human  
CA IX carbonic anhydrase domain construct

<400> 6

Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala	
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Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu	
20 25 30	
Met Pro Val His Pro Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly	
35 40 45	
Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln	
50 55 60	
Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu	
65 70 75 80	
Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu	
85 90 95	
Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly	
100 105 110	
Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu	
115 120 125	
His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val	
130 135 140	
Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr	
145 150 155 160	
Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala	
165 170 175	



Val	Leu	Ala	Ala	Phe	Leu	Glu	Glu	Gly	Pro	Glu	Glu	Asn	Ser	Ala	Tyr	
			180					185					190			
Glu	Gln	Leu	Leu	Ser	Arg	Leu	Glu	Glu	Ile	Ala	Glu	Glu	Gly	Ser	Glu	
		195					200					205				
Thr	Gln	Val	Pro	Gly	Leu	Asp	Ile	Ser	Ala	Leu	Leu	Pro	Ser	Asp	Phe	
	210				215						220					
Ser	Arg	Tyr	Phe	Gln	Tyr	Glu	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Ala	
225				230					235						240	
Gln	Gly	Val	Ile	Trp	Thr	Val	Phe	Asn	Gln	Thr	Val	Met	Leu	Ser	Ala	
			245					250					255			
Lys	Gln	Leu	His	Thr	Leu	Ser	Asp	Thr	Leu	Trp	Gly	Pro	Gly	Asp	Ser	
		260					265					270				
Arg	Leu	Gln	Leu	Asn	Phe	Arg	Ala	Thr	Gln	Pro	Leu	Asn	Gly	Arg	Val	
	275				280							285				
Ile	Glu	Ala	Ser	Phe	Pro	Ala	Gly	Val	Asp	Ser	Ser	Pro	Arg	Ala	Ala	
	290				295						300					
Glu	Pro	Val	Gln	Leu	Asn	Ser	Cys	Leu	Ala	Ala	Gly	Asp	Ile	Leu	Ala	
305				310					315						320	
Leu	Val	Phe	Gly	Leu	Leu	Phe	Ala	Val	Thr	Ser	Val	Ala	Phe	Leu	Val	
			325					330					335			
Gln	Met	Arg	Arg	Gln	His	Arg	Arg	Gly	Thr	Lys	Gly	Gly	Val	Ser	Tyr	
		340					345					350				
Arg	Pro	Ala	Glu	Val	Ala	Glu	Thr	Gly	Ala							
		355					360									

<210> 7

<211> 978

<212> DNA

<213> Artificial Sequence

<220>

<223> Coding sequence for glu-tagged human CA IX  
carbonic anhydrase domain construct

<221> CDS

<222> (1)...(978)

<400> 7

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Met	Ala	Pro	Leu	Cys	Pro	Ser	Pro	Trp	Leu	Pro	Leu	Leu	Ile	Pro	Ala	
1			5					10					15			

cct	gct	cca	ggc	ctc	act	gtg	caa	ctg	ctg	ctg	tca	ctg	ctg	ctt	ctg	96
Pro	Ala	Pro	Gly	Leu	Thr	Val	Gln	Leu	Leu	Leu	Ser	Leu	Leu	Leu	Leu	
			20				25					30				

atg	cct	gtc	cat	ccc	cag	agg	ttg	ccc	cgg	atg	cag	gag	gct	agc	gaa	144
Met	Pro	Val	His	Pro	Gln	Arg	Leu	Pro	Arg	Met	Gln	Glu	Ala	Ser	Glu	
		35				40					45					

tac	atg	cca	atg	gaa	caa	gaa	ccc	cag	aat	aat	gcc	cac	agg	gac	aaa	192
Tyr	Met	Pro	Met	Glu	Gln	Glu	Pro	Gln	Asn	Asn	Ala	His	Arg	Asp	Lys	
	50					55					60					

gaa ggg gat gac cag agt cat tgg cgc tat gga ggc gac ccg ccc tgg	240
Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp	
65 70 75 80	
ccc cgg gtg tcc cca gcc tgc gcg ggc cgc ttc cag tcc ccg gtg gat	288
Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp	
85 90 95	
atc cgc ccc cag ctc gcc gcc ttc tgc ccg gcc ctg cgc ccc ctg gaa	336
Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu	
100 105 110	
ctc ctg ggc ttc cag ctc ccg ccg ctc cca gaa ctg cgc ctg cgc aac	384
Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn	
115 120 125	
aat ggc cac agt gtg caa ctg acc ctg cct cct ggg cta gag atg gct	432
Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala	
130 135 140	
ctg ggt ccc ggg cgg gag tac cgg gct ctg cag ctg cat ctg cac tgg	480
Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp	
145 150 155 160	
ggg gct gca ggt cgt ccg ggc tcg gag cac act gtg gaa ggc cac cgt	528
Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg	
165 170 175	
ttc cct gcc gag atc cac gtg gtt cac ctc agc acc gcc ttt gcc aga	576
Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg	
180 185 190	
gtt gac gag gcc ttg ggg cgc ccg gga ggc ctg gcc gtg ttg gcc gcc	624
Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala	
195 200 205	
ttt ctg gag gag ggc ccg gaa gaa aac agt gcc tat gag ctc cac acc	672
Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Leu His Thr	
210 215 220	
ctc tct gac acc ctg tgg gga cct ggt gac tct cgg cta cag ctg aac	720
Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu Asn	
225 230 235 240	
ttc cga gcg acg cag cct ttg aat ggg cga gtg att gag gcc tcc ttc	768
Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser Phe	
245 250 255	
cct gct gga gtg gac agc agt cct cgg gct gct gag cca gtc cag ctg	816
Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala Glu Pro Val Gln Leu	
260 265 270	
aat tcc tgc ctg gct gct ggt gac atc cta gcc ctg gtt ttt ggc ctc	864
Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala Leu Val Phe Gly Leu	
275 280 285	

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ctt ttt gct gtc acc agc gtc gcg ttc ctt gtg cag atg aga agg cag 912
Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln
290 295 300

cac aga agg gga acc aaa ggg ggt gtg agc tac cgc cca gca gag gta 960
His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val
305 310 315 320

gcc gag act gga gcc tag 978
Ala Glu Thr Gly Ala *
325

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```

<210> 8
<211> 325
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> Polypeptide encoded by coding sequence for
      glu-tagged human CA IX carbonic anhydrase domain
      construct

```

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<400> 8
Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
1 5 10 15
Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Ser Leu Leu Leu
20 25 30
Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Ala Ser Glu
35 40 45
Tyr Met Pro Met Glu Gln Glu Pro Gln Asn Asn Ala His Arg Asp Lys
50 55 60
Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp
65 70 75 80
Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp
85 90 95
Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu
100 105 110
Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn
115 120 125
Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala
130 135 140
Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp
145 150 155 160
Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg
165 170 175
Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg
180 185 190
Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala
195 200 205
Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Leu His Thr
210 215 220
Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu Asn
225 230 235 240
Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser Phe
245 250 255

```

Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala Glu Pro Val Gln Leu  
260 265 270  
Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala Leu Val Phe Gly Leu  
275 280 285  
Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln  
290 295 300  
His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val  
305 310 315 320  
Ala Glu Thr Gly Ala  
325

<210> 9

<211> 978

<212> DNA

<213> Artificial Sequence

<220>

<223> Coding sequence for glu-tagged mutant human CA IX  
carbonic anhydrase domain construct

<221> CDS

<222> (1)...(978)

<400> 9

atg gct ccc ctg tgc ccc agc ccc tgg ctc cct ctg ttg atc ccg gcc	48
Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala	
1 5 10 15	
cct gct cca ggc ctc act gtg caa ctg ctg ctg tca ctg ctg ctt ctg	96
Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu	
20 25 30	
atg cct gtc cat ccc cag agg ttg ccc cgg atg cag gag gct agc gaa	144
Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Ala Ser Glu	
35 40 45	
tac atg cca atg gaa caa gaa ccc cag aat aat gcc cac agg gac aaa	192
Tyr Met Pro Met Glu Gln Glu Pro Gln Asn Asn Ala His Arg Asp Lys	
50 55 60	
gaa ggg gat gac cag agt cat tgg cgc tat gga ggc gac ccg ccc tgg	240
Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp	
65 70 75 80	
ccc cgg gtg tcc cca gcc tgc gcg ggc cgc ttc cag tcc ccg gtg gat	288
Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp	
85 90 95	
atc cgc ccc cag ctc gcc gcc ttc tgc ccg gcc ctg cgc ccc ctg gaa	336
Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu	
100 105 110	
ctc ctg ggc ttc cag ctc ccg ccg ctc cca gaa ctg cgc ctg cgc aac	384
Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn	
115 120 125	

aat ggc cac agt gtg caa ctg acc ctg cct cct ggg cta gag atg gct	432
Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala	
130 135 140	
ctg ggt ccc ggg cgg gag tac cgg gct ctg cag ctg caa ctg cag tgg	480
Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu Gln Leu Gln Trp	
145 150 155 160	
ggg gct gca ggt cgt ccg ggc tcg gag cac act gtg gaa ggc cac cgt	528
Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg	
165 170 175	
ttc cct gcc gag atc caa gtg gtt cac ctc agc acc gcc ttt gcc aga	576
Phe Pro Ala Glu Ile Gln Val Val His Leu Ser Thr Ala Phe Ala Arg	
180 185 190	
gtt gac gag gcc ttg ggg cgc ccg gga ggc ctg gcc gtg ttg gcc gcc	624
Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala	
195 200 205	
ttt ctg gag gag ggc ccg gaa gaa aac agt gcc tat gag ctc cac acc	672
Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Leu His Thr	
210 215 220	
ctc tct gac acc ctg tgg gga cct ggt gac tct cgg cta cag ctg aac	720
Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu Asn	
225 230 235 240	
ttc cga gcg acg cag cct ttg aat ggg cga gtg att gag gcc tcc ttc	768
Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser Phe	
245 250 255	
cct gct gga gtg gac agc agt cct cgg gct gct gag cca gtc cag ctg	816
Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala Glu Pro Val Gln Leu	
260 265 270	
aat tcc tgc ctg gct gct ggt gac atc cta gcc ctg gtt ttt ggc ctc	864
Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu Ala Leu Val Phe Gly Leu	
275 280 285	
ctt ttt gct gtc acc agc gtc gcg ttc ctt gtg cag atg aga agg cag	912
Leu Phe Ala Val Thr Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln	
290 295 300	
cac aga agg gga acc aaa ggg ggt gtg agc tac cgc cca gca gag gta	960
His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val	
305 310 315 320	
gcc gag act gga gcc tag	978
Ala Glu Thr Gly Ala *	
325	

<210> 10  
 <211> 325  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Polypeptide encoded by coding sequence for  
glu-tagged mutant human CA IX carbonic anhydrase  
domain construct

<400> 10

Met	Ala	Pro	Leu	Cys	Pro	Ser	Pro	Trp	Leu	Pro	Leu	Leu	Ile	Pro	Ala
1				5					10					15	
Pro	Ala	Pro	Gly	Leu	Thr	Val	Gln	Leu	Leu	Ser	Leu	Leu	Leu	Leu	
			20					25					30		
Met	Pro	Val	His	Pro	Gln	Arg	Leu	Pro	Arg	Met	Gln	Glu	Ala	Ser	Glu
		35					40					45			
Tyr	Met	Pro	Met	Glu	Gln	Glu	Pro	Gln	Asn	Asn	Ala	His	Arg	Asp	Lys
	50					55					60				
Glu	Gly	Asp	Asp	Gln	Ser	His	Trp	Arg	Tyr	Gly	Gly	Asp	Pro	Pro	Trp
65					70					75					80
Pro	Arg	Val	Ser	Pro	Ala	Cys	Ala	Gly	Arg	Phe	Gln	Ser	Pro	Val	Asp
			85						90					95	
Ile	Arg	Pro	Gln	Leu	Ala	Ala	Phe	Cys	Pro	Ala	Leu	Arg	Pro	Leu	Glu
			100					105					110		
Leu	Leu	Gly	Phe	Gln	Leu	Pro	Pro	Leu	Pro	Glu	Leu	Arg	Leu	Arg	Asn
		115					120					125			
Asn	Gly	His	Ser	Val	Gln	Leu	Thr	Leu	Pro	Pro	Gly	Leu	Glu	Met	Ala
	130					135					140				
Leu	Gly	Pro	Gly	Arg	Glu	Tyr	Arg	Ala	Leu	Gln	Leu	Gln	Leu	Gln	Trp
145					150					155					160
Gly	Ala	Ala	Gly	Arg	Pro	Gly	Ser	Glu	His	Thr	Val	Glu	Gly	His	Arg
				165					170					175	
Phe	Pro	Ala	Glu	Ile	Gln	Val	Val	His	Leu	Ser	Thr	Ala	Phe	Ala	Arg
			180					185					190		
Val	Asp	Glu	Ala	Leu	Gly	Arg	Pro	Gly	Gly	Leu	Ala	Val	Leu	Ala	Ala
		195					200					205			
Phe	Leu	Glu	Glu	Gly	Pro	Glu	Glu	Asn	Ser	Ala	Tyr	Glu	Leu	His	Thr
	210					215					220				
Leu	Ser	Asp	Thr	Leu	Trp	Gly	Pro	Gly	Asp	Ser	Arg	Leu	Gln	Leu	Asn
225					230					235					240
Phe	Arg	Ala	Thr	Gln	Pro	Leu	Asn	Gly	Arg	Val	Ile	Glu	Ala	Ser	Phe
			245						250					255	
Pro	Ala	Gly	Val	Asp	Ser	Ser	Pro	Arg	Ala	Ala	Glu	Pro	Val	Gln	Leu
			260					265					270		
Asn	Ser	Cys	Leu	Ala	Ala	Gly	Asp	Ile	Leu	Ala	Leu	Val	Phe	Gly	Leu
		275					280					285			
Leu	Phe	Ala	Val	Thr	Ser	Val	Ala	Phe	Leu	Val	Gln	Met	Arg	Arg	Gln
	290					295					300				
His	Arg	Arg	Gly	Thr	Lys	Gly	Gly	Val	Ser	Tyr	Arg	Pro	Ala	Glu	Val
305					310					315					320
Ala	Glu	Thr	Gly	Ala											
				325											